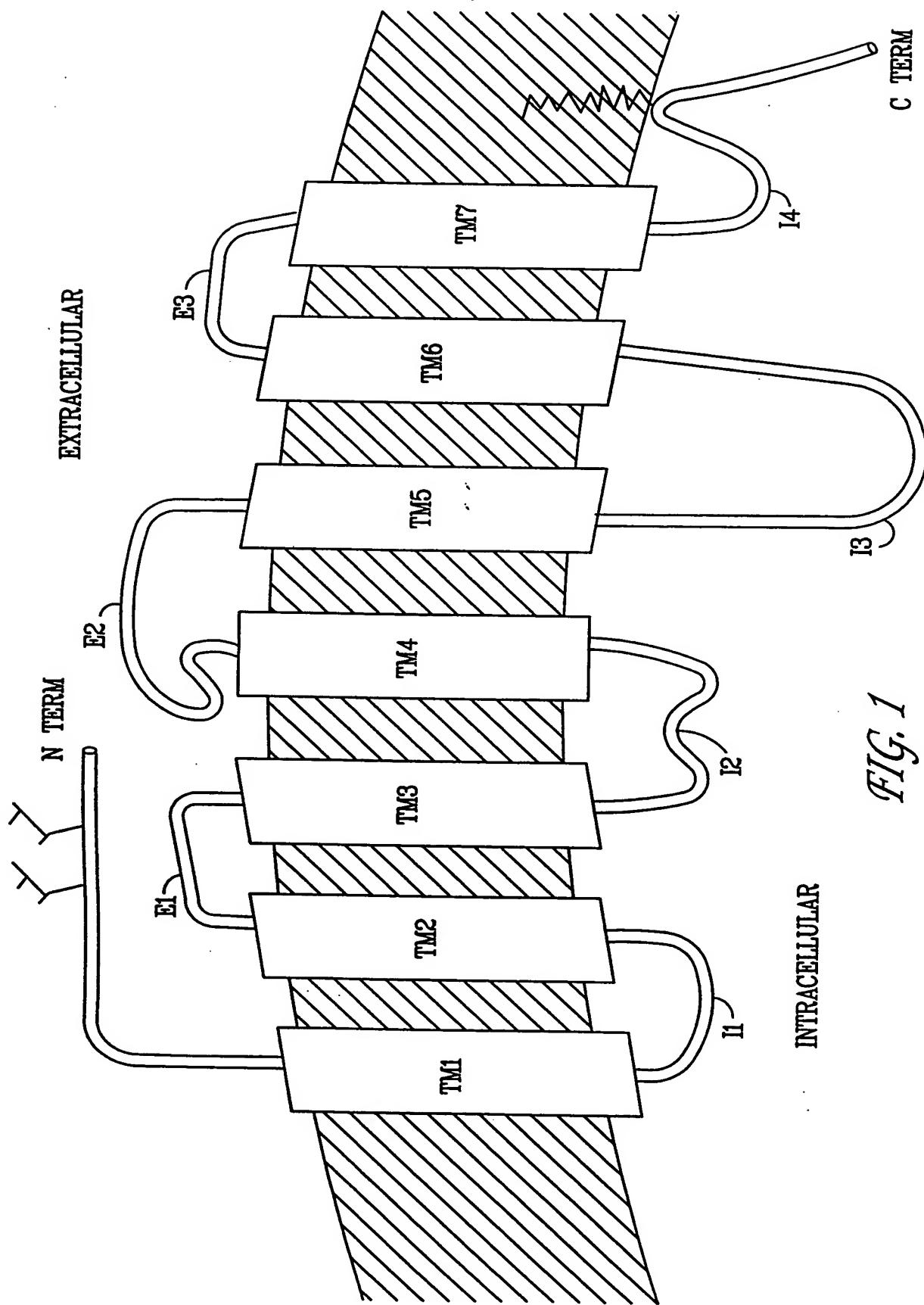


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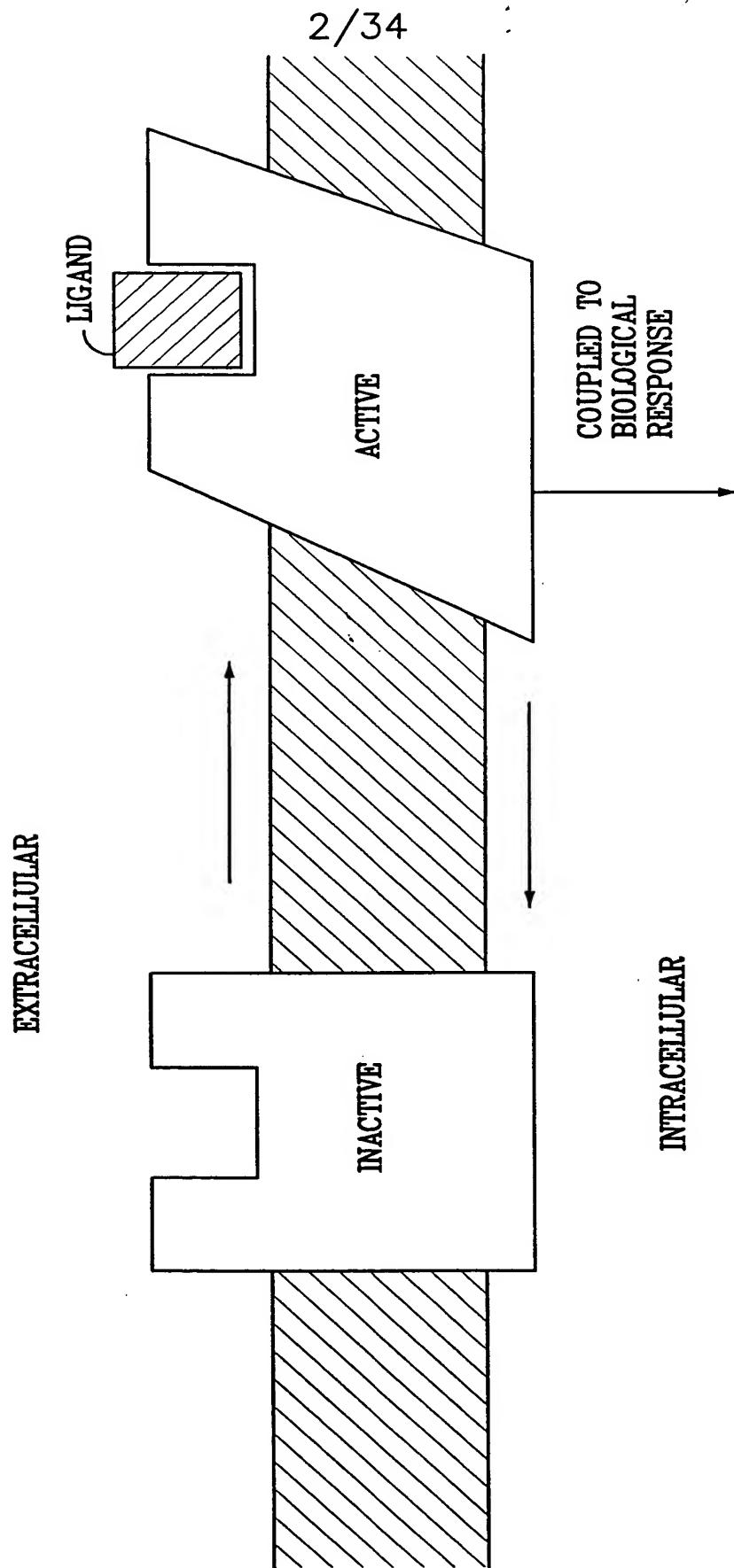
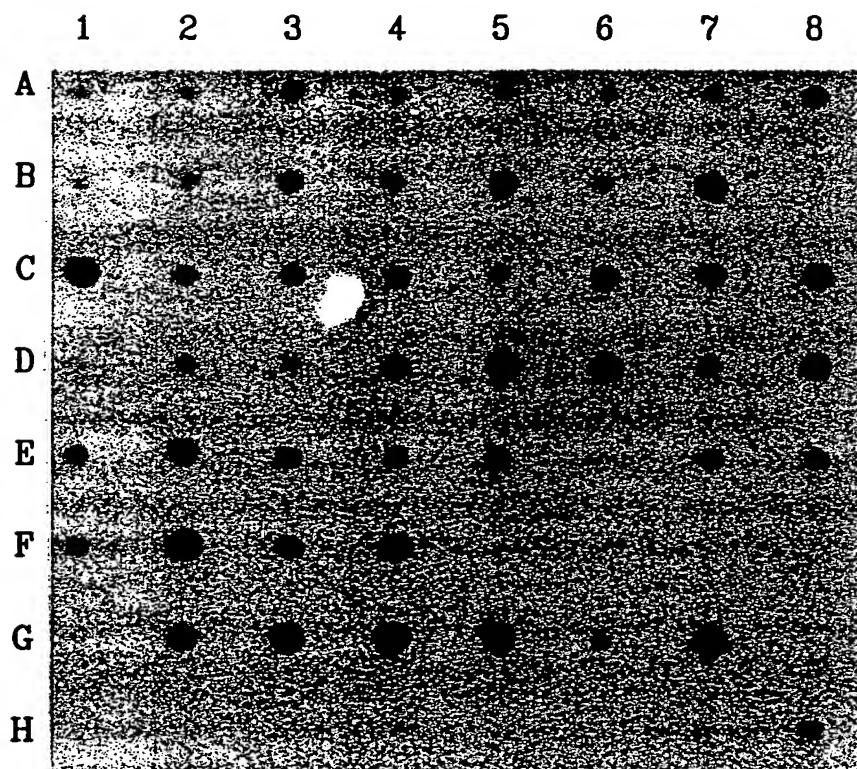


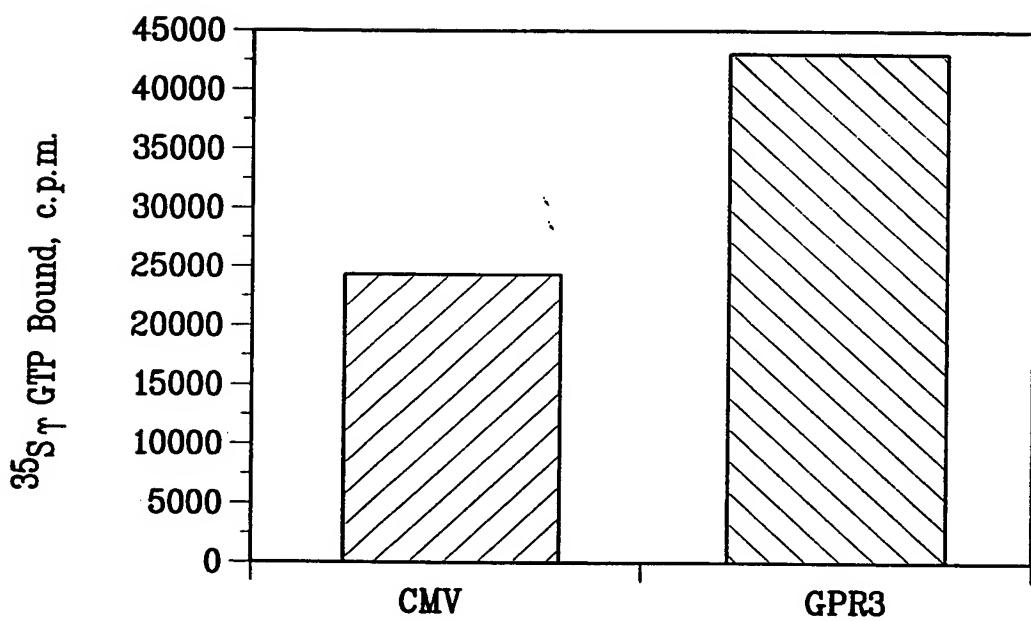
FIG. 2

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*FIG. 3*

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*FIG. 4*

Figure 5A

10 30 40

1 **M M** - - - - - **W G A G S** SEQ.ID.NO.: 46  
 1 **M N** **A S A S L N D** **S Q V V V V V A E G A A A A A T A A G G P D T G E** **W G P P A** SEQ.ID.NO.: 47  
 1 **M N** - - - - - **E D L K V N L** - - - - - **S G L** SEQ.ID.NO.: 48

50 60 70 80

8 **P L A W L S I A G S G** **G N V N V S S V G P A E G P T G P** **P A A P L P S P K A W D V V L** SEQ.ID.NO.: 46  
 41 **A A A - L G A G G G A N G S L E L S S Q L S A G P P G L L L P A V N P W D V L L** SEQ.ID.NO.: 47  
 13 **P R D Y L D A A A A E N I S A A V S S R V P A V E P E P E L - V V N P W D I V L** SEQ.ID.NO.: 48

90 100 110 120

48 **C I S G T L V S C E N A L V V A I I V G T P A F R A P M F L L V G S L A V A D L** SEQ.ID.NO.: 46  
 80 **C V S G T V I A G E N A L V V A L I A S T P A L R T P M F V L V G S L A T A D L** SEQ.ID.NO.: 47  
 52 **C T S G T L I S C E N A I V V L I I F H N P S L R A P M F L L I G S L A L A D L** SEQ.ID.NO.: 48

130 140 150 160

88 **L A G L G L V L H F A A V F C I G S A E M S L V L V G V L A M A F T A S I G S L** SEQ.ID.NO.: 46  
 120 **L A G C G L I L H F V F Q Y L V P S E T V S L L T V G F L V A S F A A S V S S L** SEQ.ID.NO.: 47  
 92 **L A G I G L I T N F V F A Y L L Q S E A T K L V T I G L I V A S F S A S V C S L** SEQ.ID.NO.: 48

170 180 190 200

128 **L A I T V D R Y L S L Y N A L T Y Y S E T T V T R T Y V M L A L V W G G A L G L** SEQ.ID.NO.: 46  
 160 **L A I T V D R Y L S L Y N A L T Y Y S R R T L L G V H L L L A A T W T V S L G L** SEQ.ID.NO.: 47  
 132 **L A I T V D R Y L S L Y Y A L T Y H S E R T V T F T Y V M L V M L W G T S I C L** SEQ.ID.NO.: 48

210 220 230 240

168 **G L L P V L A W N C L D G L T T C G V V Y P L S K N H L V V L A I A F F M V F G** SEQ.ID.NO.: 46  
 200 **G L L P V L G W N C L A E R A A C S V V R P L A R S H V A L L S A A F F M V F G** SEQ.ID.NO.: 47  
 172 **G L L P V M G W N C L R D E S T C S V V R P L T K N N A A I L S V S F L F M F A** SEQ.ID.NO.: 48

250 260 270 280

208 **I M L Q L Y A Q I C R I V C R H A Q Q I A L Q R H L L P A S H Y V A T R K G I A** SEQ.ID.NO.: 46  
 240 **I M L H L Y V R I C Q V V W R H A H Q I A L Q Q H C L A P P H L A A T R K G V G** SEQ.ID.NO.: 47  
 212 **L M L Q L Y I Q I C K I V M R H A H Q I A L Q H H F L A T S H Y V T T R K G V S** SEQ.ID.NO.: 48

290 300 310 320

248 **T L A V V L G A F A A C W L P F T V Y C L L G D A H S P P L Y T Y L T L L P A T** SEQ.ID.NO.: 46  
 280 **T L A V V L G T F G A S W L P F A I Y C V V G S H E D P A V Y T Y A T L L P A T** SEQ.ID.NO.: 47  
 252 **T L A I I L G T F A A C W M P F T L Y S L I A D Y T Y P S I Y T Y A T L L P A T** SEQ.ID.NO.: 48

330 340 350 360

288 **Y N S M I N P I I Y A F R N Q D V Q K V L W A V C C C C S S S K I P F R S R S P** SEQ.ID.NO.: 46  
 320 **Y N S M I N P I I Y A F R N Q E I Q R A L W L L L C G C F Q S K V P F R S R S P** SEQ.ID.NO.: 47  
 292 **Y N S T I N P V I Y A F R N Q E I Q K A L C L I C C G C I P S S L A Q R A R S P** SEQ.ID.NO.: 48

328 **S D V** SEQ.ID.NO.: 46  
 360 **S E V** SEQ.ID.NO.: 47  
 332 **S D V** SEQ.ID.NO.: 48

Figure 5B

	10	20	30	40	
1	M N E S R W T E W R I L	N M S S G I V N	V S E R H S C P L	G F G H Y S V V D V C	SEQ.ID.NO.: 19
1	M N S T - - - - L	D - - - - G N	Q S S H P F C L	L A F G Y - - - -	SEQ.ID.NO.: 15
	50	60	70	80	
41	I F E T V V I V L L T F L I I - - - - A G N	L T V I F V F H C A P L L I H	SEQ.ID.NO.: 19		
22	- L E T V N F C L I E V L I I V F L T V L I I S G N I	I V I F V F H C A P L L N	SEQ.ID.NO.: 15		
	90	100	110	120	
73	H Y T T S Y F I Q T M A Y A D L F V G V S C L V P T	L S L L H Y S T G V H E S L	SEQ.ID.NO.: 19		
61	H H T T S Y F I Q T M A Y A D L F V G V S C V V P S	L S L L H H P L P V E E S L	SEQ.ID.NO.: 15		
	130	140	150	160	
113	T C Q V F G Y I I S V L K S V S M A C L A C I S V D R Y L	A I T K P L S Y N Q L	SEQ.ID.NO.: 19		
101	T C Q I F G F V V S V L K S V S M A S L A C I S I D R Y I	A I T K P L T Y N T L	SEQ.ID.NO.: 15		
	170	180	190	200	
153	V T P C R L R I C I I L I W I Y S C L I F L P S F F G	W G K P G Y H G D I F E W	SEQ.ID.NO.: 19		
141	V T P W R L R I C I F L I W L Y S T L V F L P S F F H	W G K P G Y H G D V F E Q W	SEQ.ID.NO.: 15		
	210	220	230	240	
193	C A T S W I L T S A Y F T G F I V C L L Y A P A A F V	V C F T Y F H I F K I C R Q	SEQ.ID.NO.: 19		
181	C A E S W H T D S Y F T L F I V M M L Y A P A A L I V	C F T Y F N I F R I C Q Q	SEQ.ID.NO.: 15		
	250	260	270	280	
233	H T K E I N D R R A R F P S H E V D S S R E T G H S P	P D R R Y A M V L F R I T S	SEQ.ID.NO.: 19		
221	H T K D I S E R Q A R F S S Q S G E T G - E V Q A C P	D K R Y A M V L F R I T S	SEQ.ID.NO.: 15		
	290	300	310	320	
273	V F Y M L W L P Y I I Y F L L E S S R V L D N P T L S	F L T T W L A I S N S F C	SEQ.ID.NO.: 19		
260	V F Y I L W L P Y I I Y F L L E S S T G H S N R F A S	F L T T W L A I S N S F C	SEQ.ID.NO.: 15		
	330	340	350	360	
313	N C V I Y S L S N S V F R L G L R R L S E T M C T S C M	C V K D Q E A Q E P - -	SEQ.ID.NO.: 19		
300	N C V I Y S L S N S V F Q R G L K R L S G A M C T S C -	AS Q T T A N D P Y T	SEQ.ID.NO.: 15		
	370				
351	- K P R K R A N S C S I				SEQ.ID.NO.: 19
338	V R S K G P L N G C H I				SEQ.ID.NO.: 15

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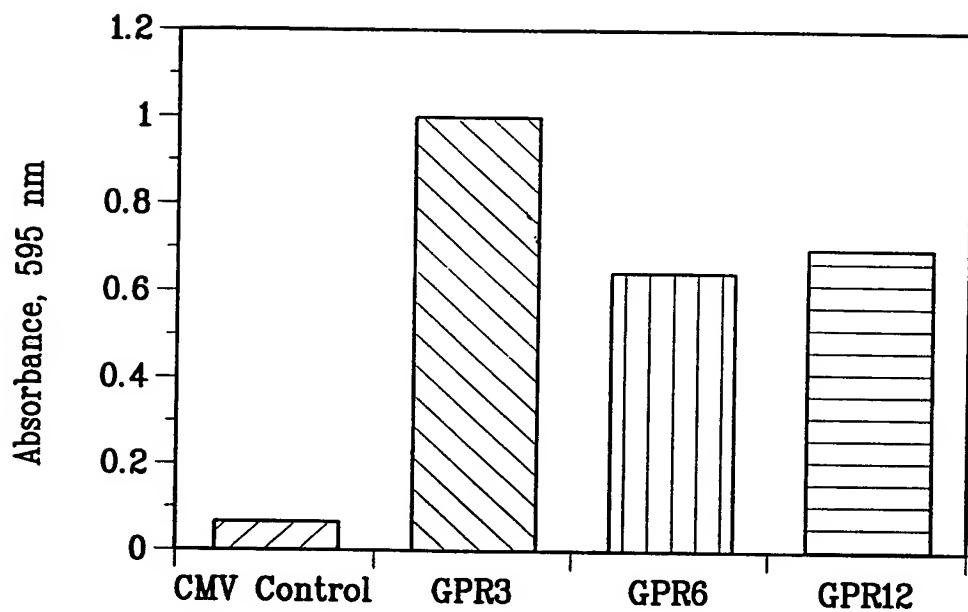
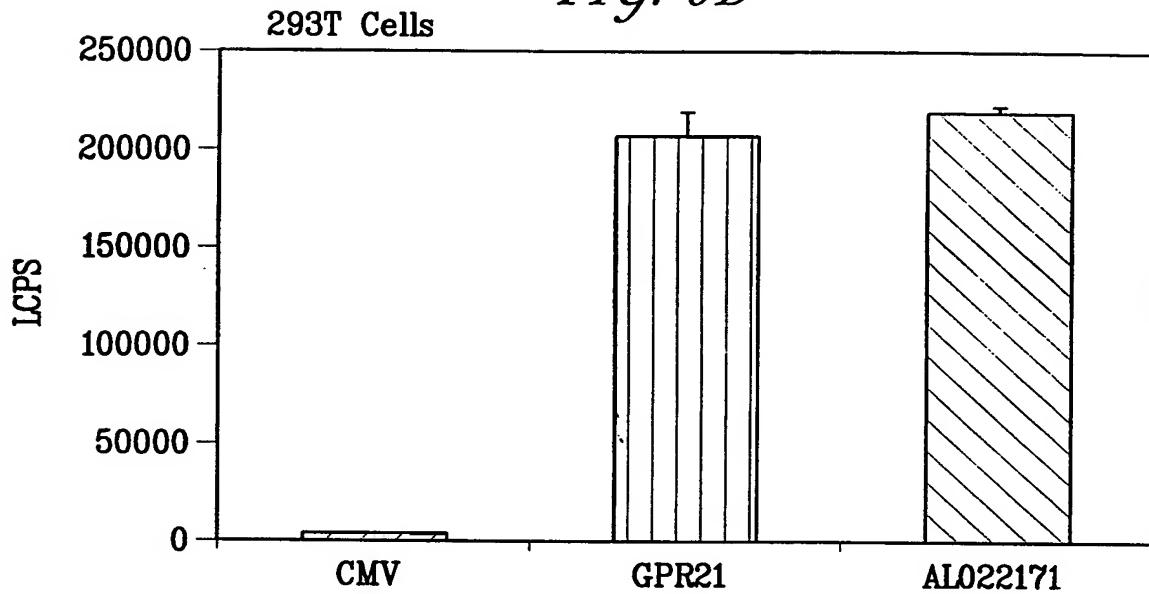


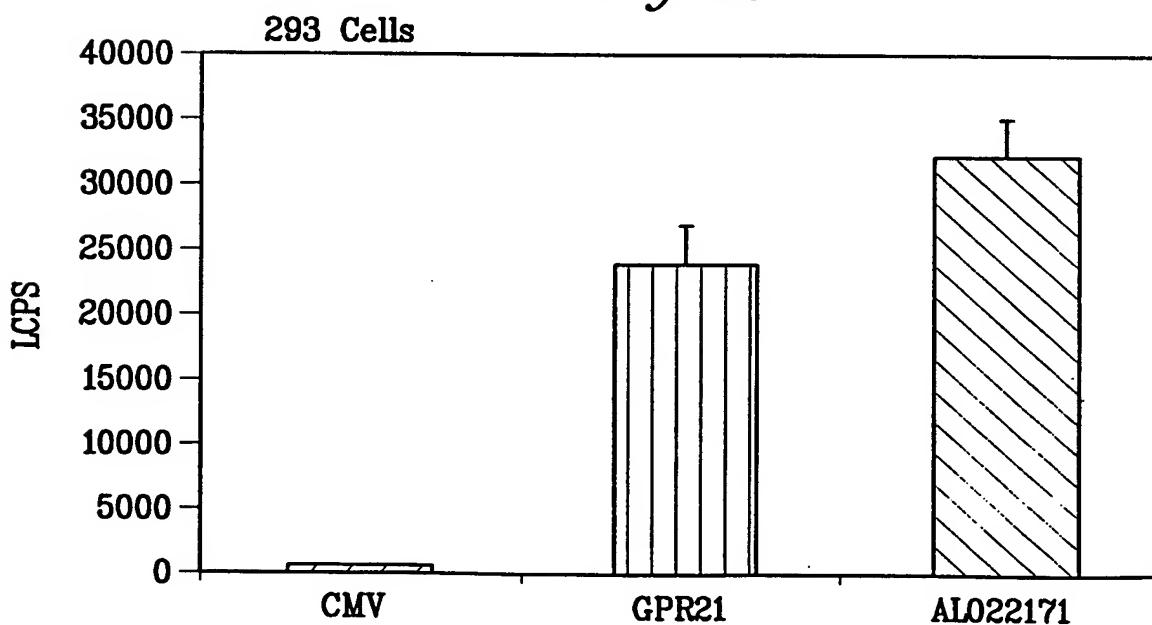
FIG. 6A

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*FIG. 6B*

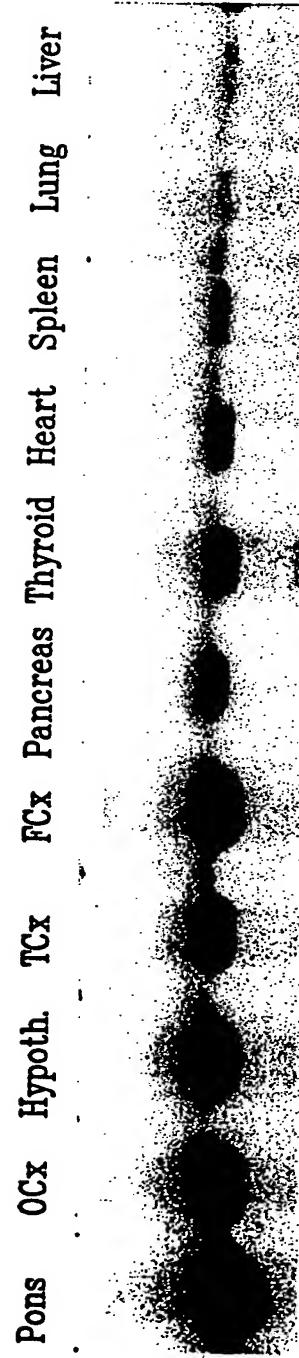


*FIG. 6C*



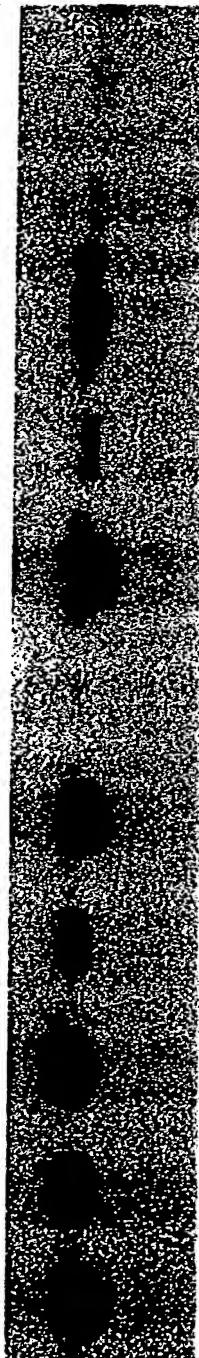
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FIG. 7A



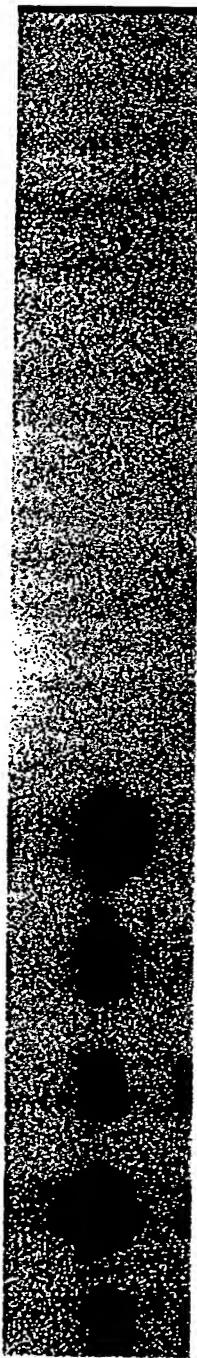
GPR3

FIG. 7B



GPR6

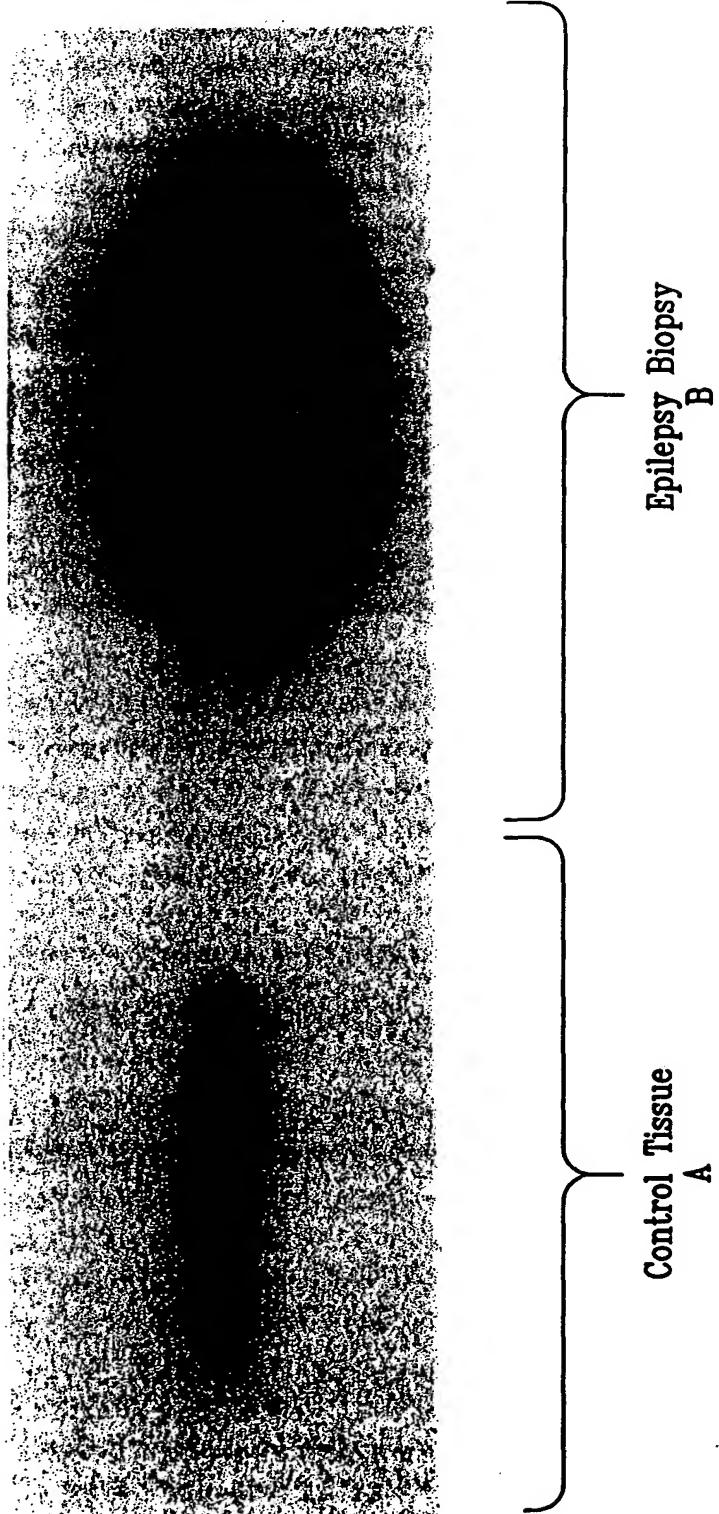
FIG. 7C



GPR12

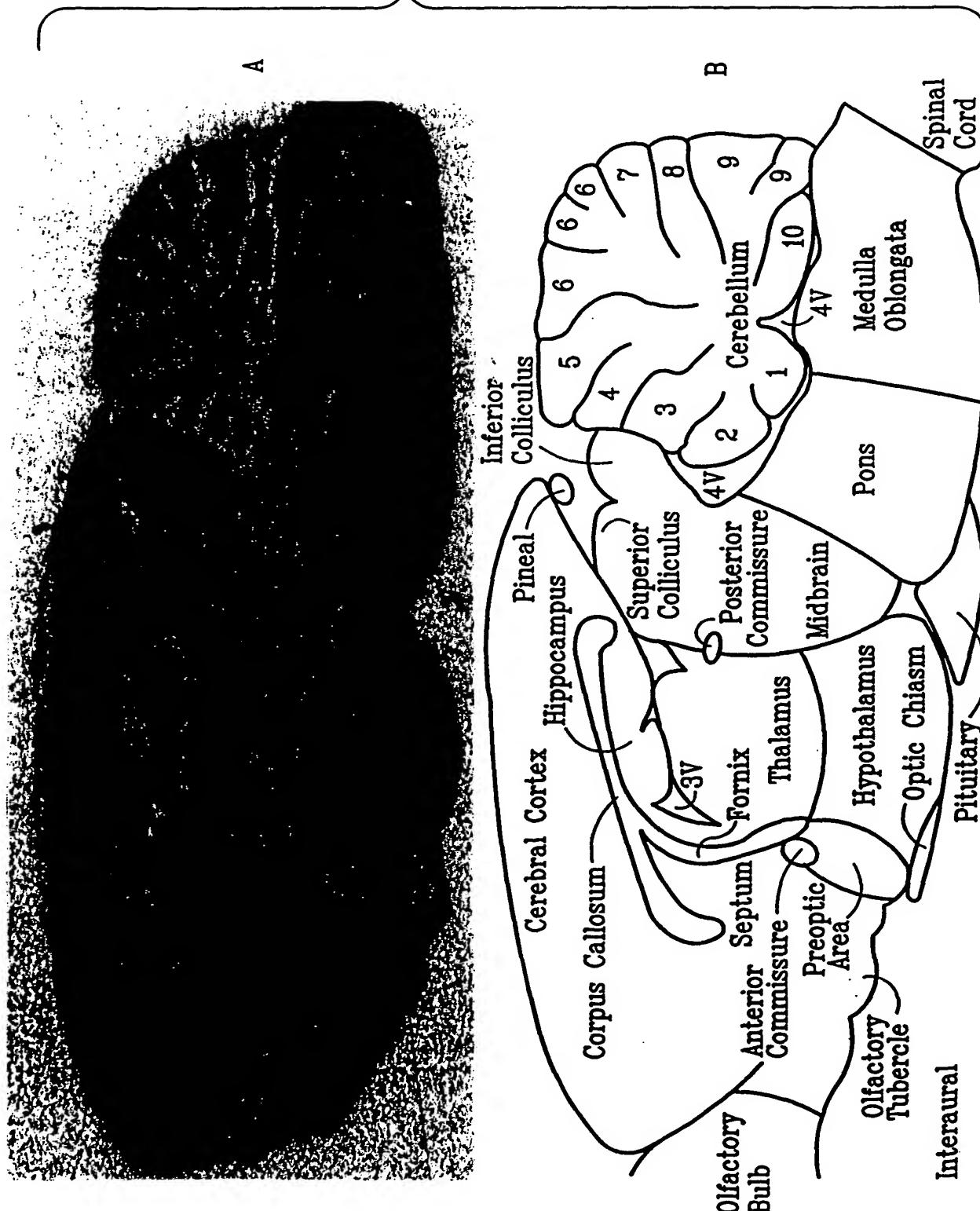
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FIG. 8



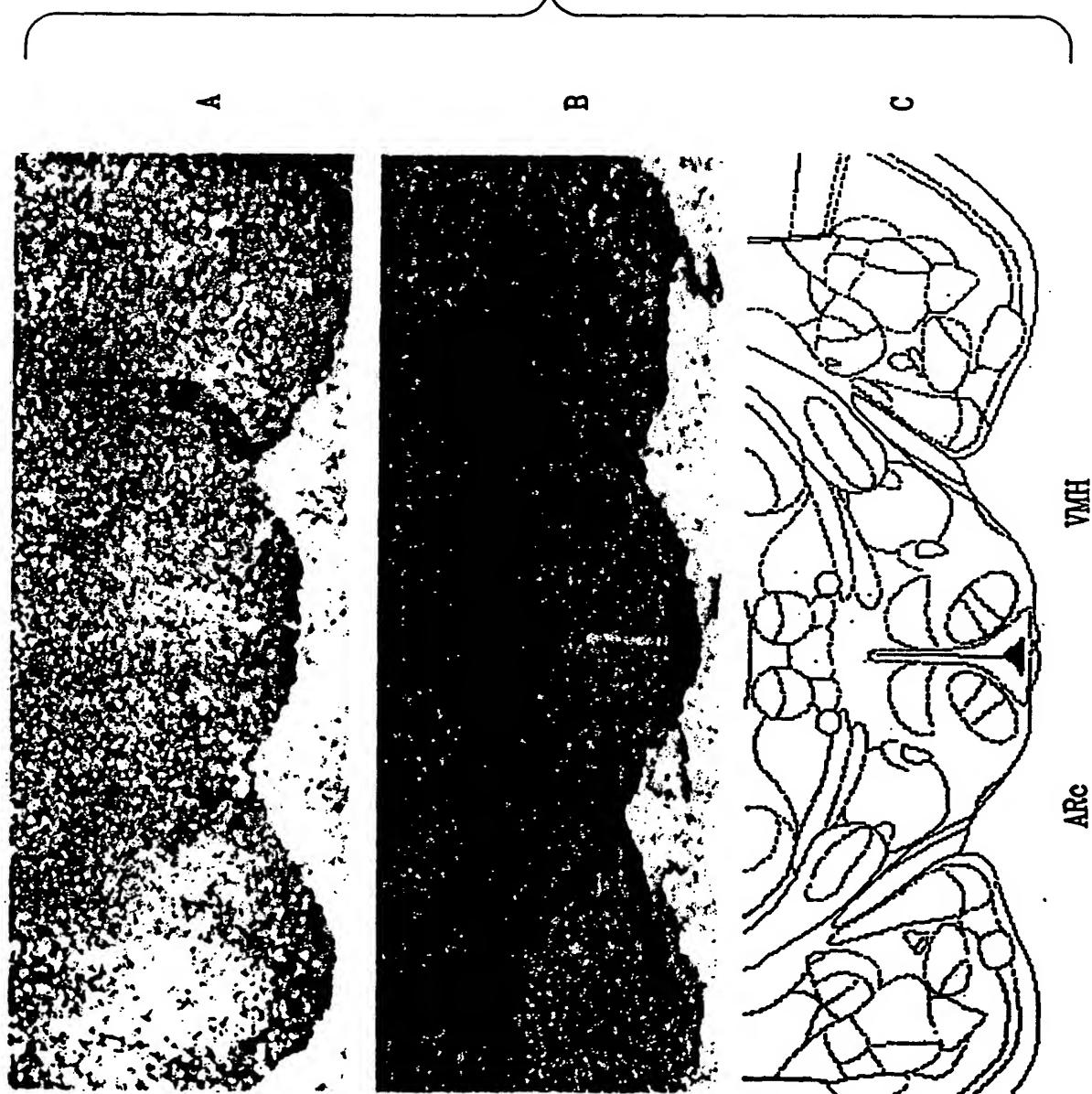
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FIG. 9



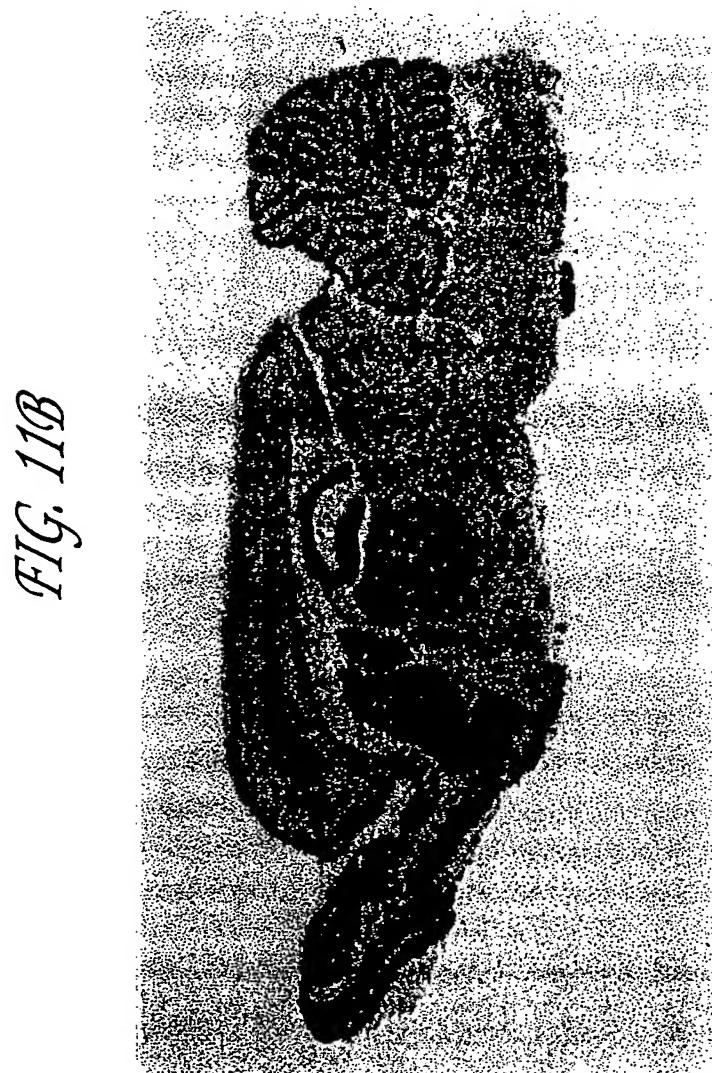
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FIG. 10



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*FIG. 11A*



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FIG. 11D

Hippocampus

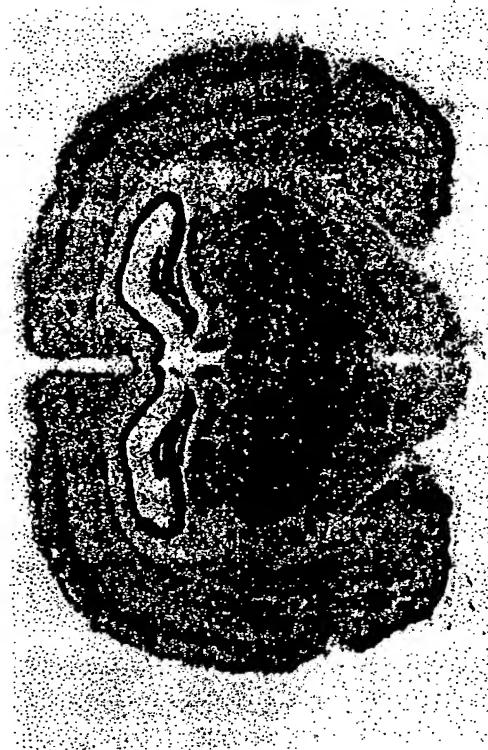


FIG. 11C

Frontal Cortex



Lateral Septum

FIG. 11E



Cortical Amygdaloid  
Nucleus

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FIG. 11F

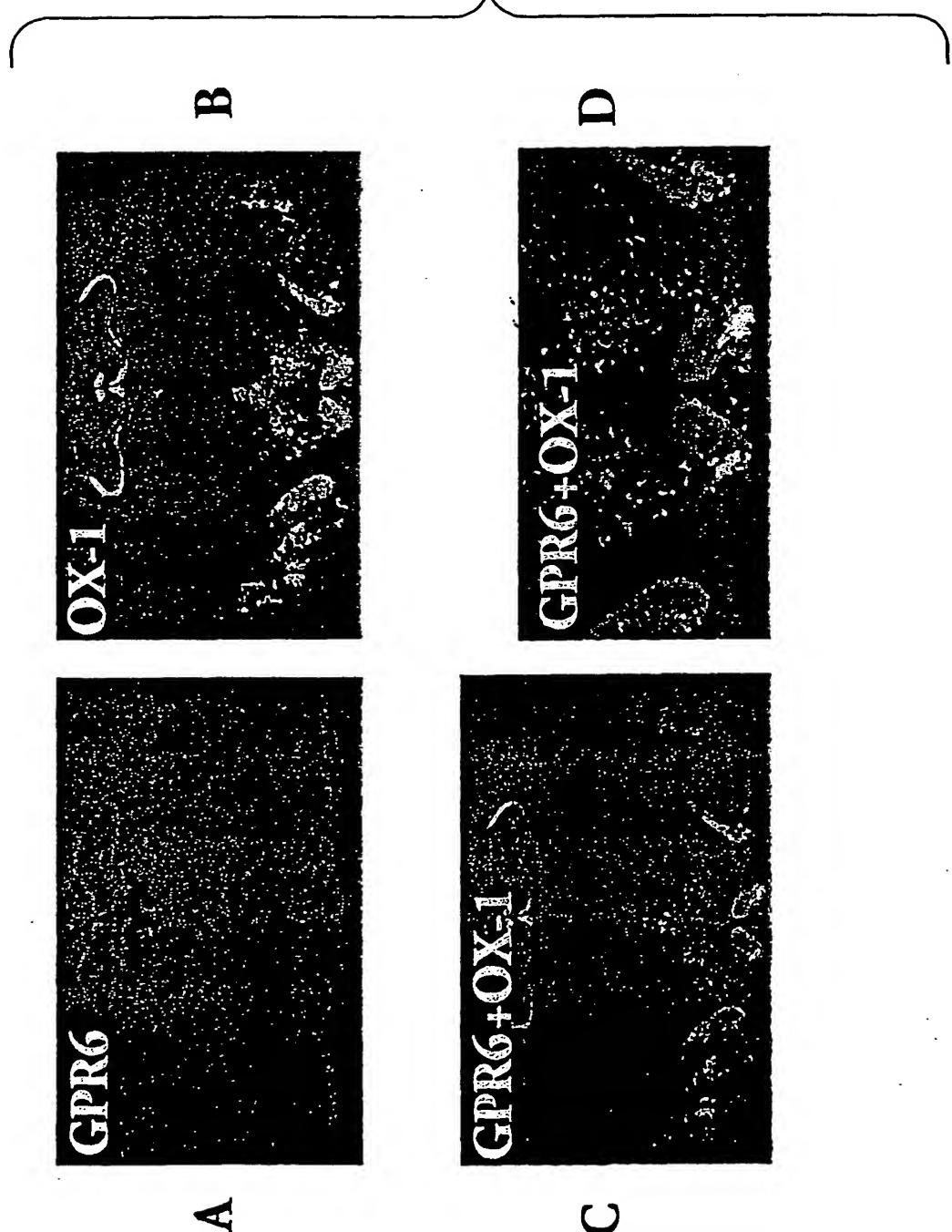


VTA

Substantia Nigra  
(compacta)

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FIG. 12

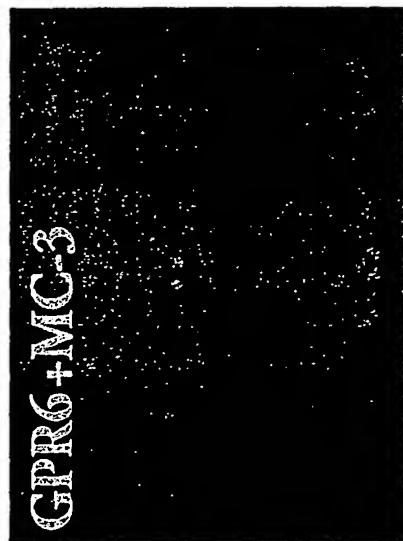
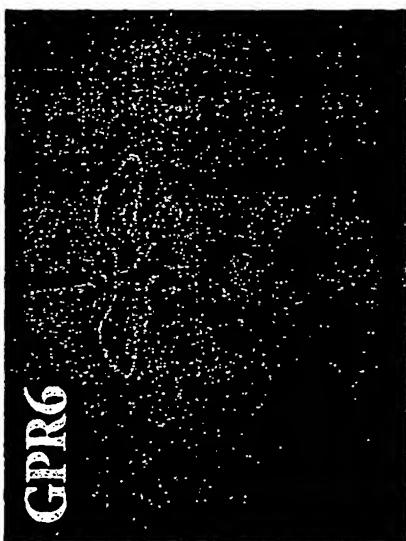
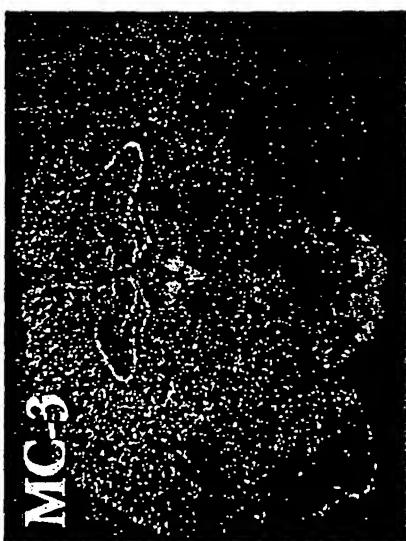


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FIG. 13

B

D



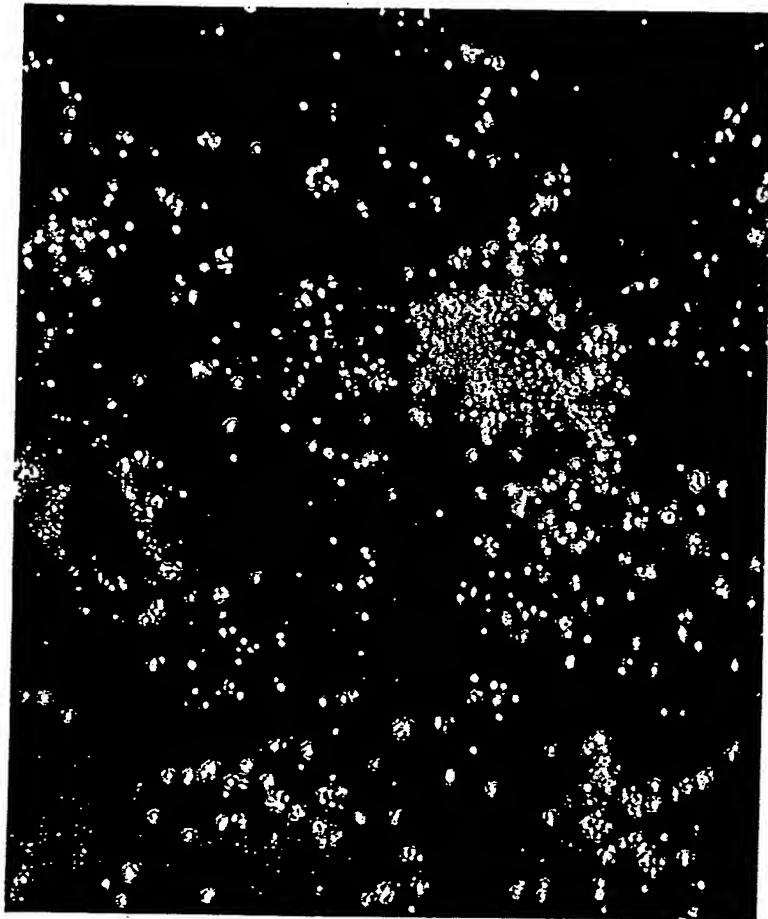
A

C

Attorney Docket: 5.US10.CON Filing Date: Herewith  
Attorney Name: Michael P. Straher Telephone: 215-665-2000  
"Endogenous, Constitutively Activated G Protein-Coupled  
Receptors"; Dominic P. Behan et al.  
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*FIG. 14*



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FIG. 15

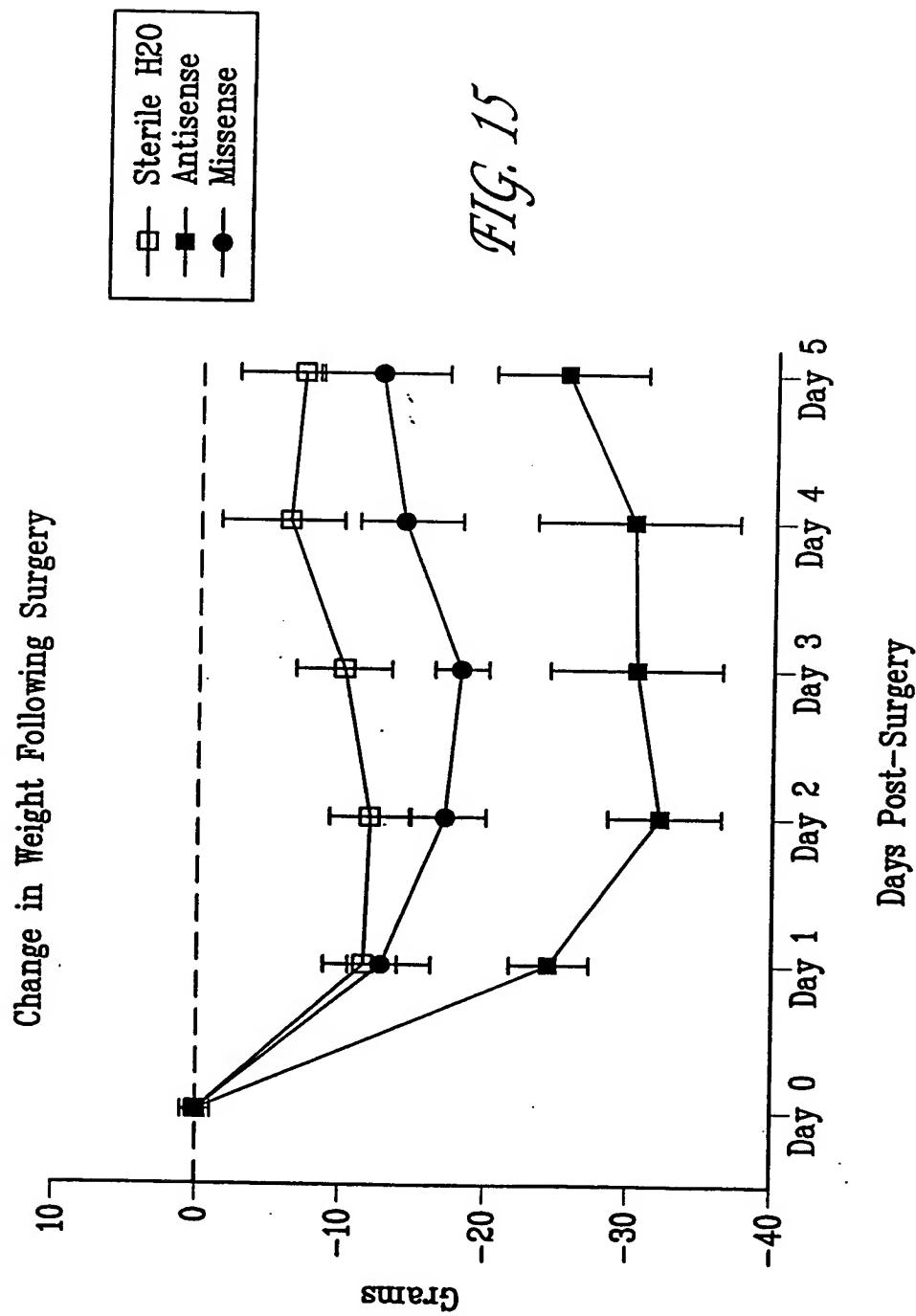
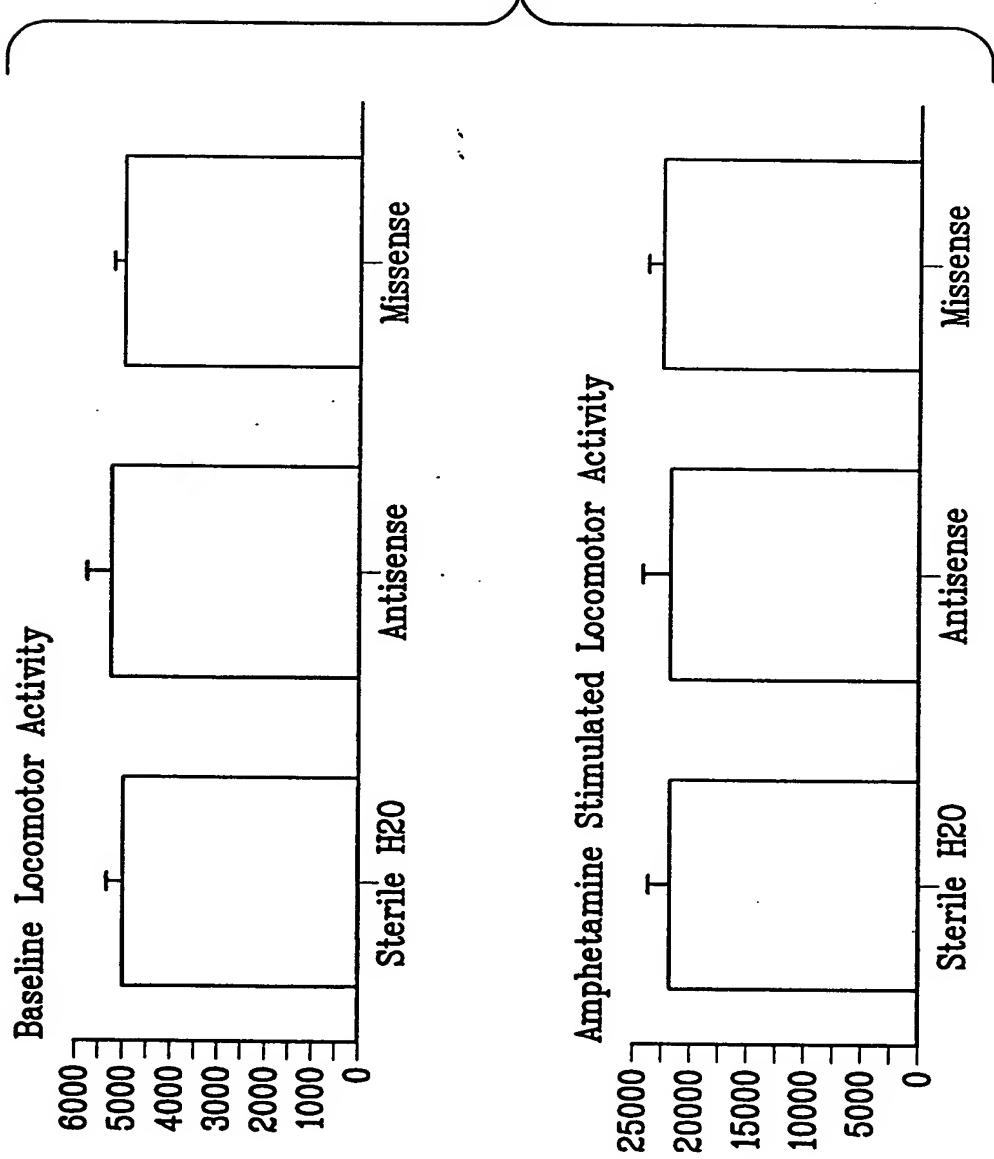


FIG. 16

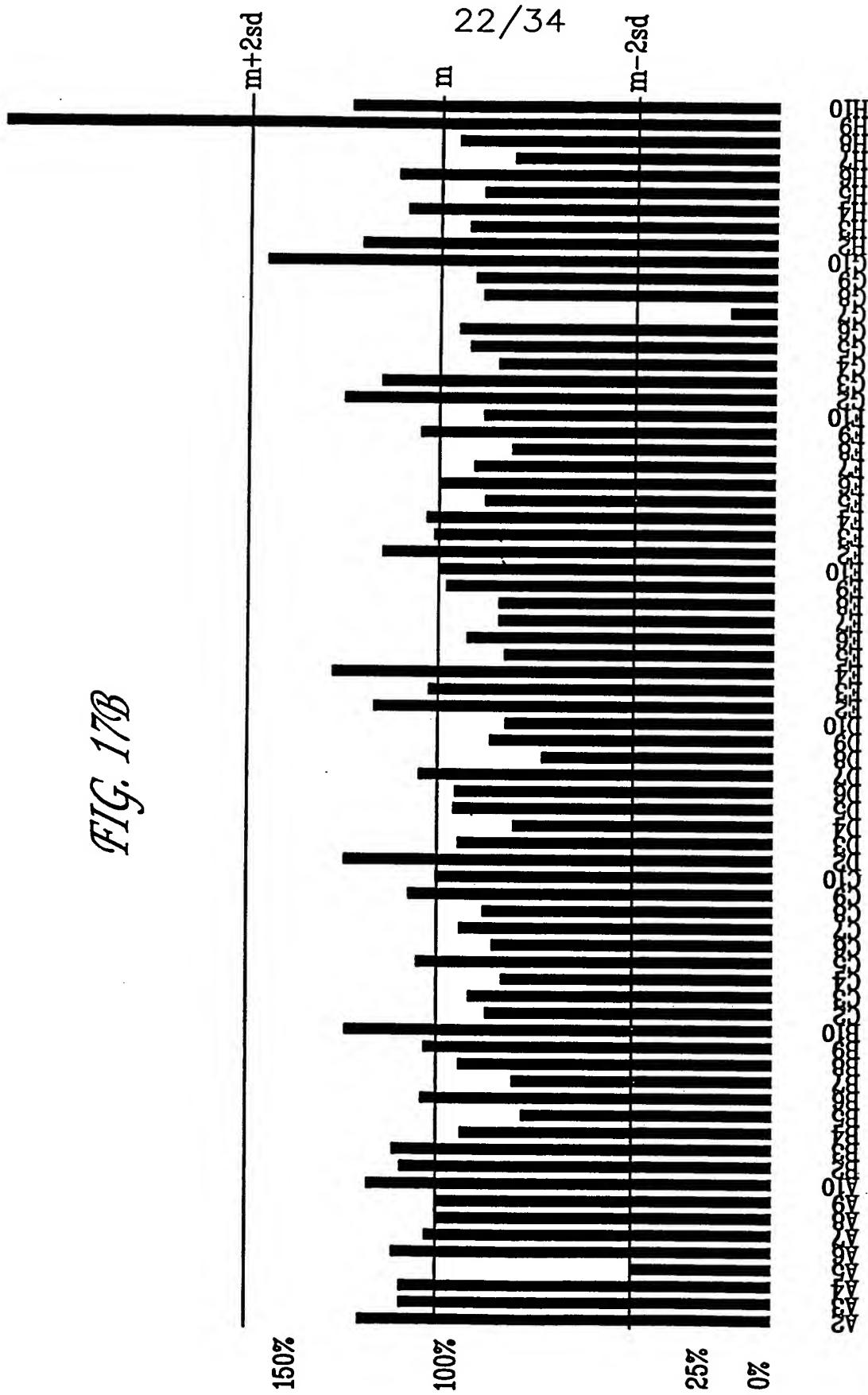


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FIG. 17A

FIG. 17B



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Pst I  
 Ava I  
 Nci I  
 EcoR V  
 Hind III  
 EcoR I  
 Nci I  
 Sma I  
 BamH I  
 Spe I  
 Xba I  
 BsrB I  
 Not I  
 Hae III  
 Sac II  
 BstX I  
 Sac I

AAGCTGATATCGAATTCTCGAGCCCCGGATCCACTAGTTCTAGACCGGCCACCGCGGTGGACCTCCAGCTTT 80  
 TTCTGAAGCTATAGCTAAGGACGTCGGGCCCCCTAGGTGATCAAGATCTCGCCGGCGTGGCGCACCTCGAGGTGCAAAAA

K L D I E F L Q F G G S T S R A A P T A V E L Q L L  
 S L I S N S C S P G D P L V L E R P R W S S Q S F  
 Q A Y R I P A A R G I H F S G R H R G G A P A F  
 L S S I S N R C G P P D V L E L A A A V A T S S W S K  
 A Q Y R I G A A R P I W N L P R W R P P A G A K

BssH II

GTTCCCTTTAGTGAGGGTTAATTGCGCGCTAGAGGATCTTGTGAAGGAACCTTACTTCTGTGGTGTGACATAATTGGAC 160  
 CAAGGGAAATCACTCCCAATTAAACGCGCGATCTCCTAGAAACACTTCTTGAATGAAGACACCAACTGTATTAACCTG  
 C F P L V R V N C A L E D L C E G T L L W C D I I G  
 S P L V G L I A R R I F V K E P L Y F C G V T H N W T  
 V P F S E G L R A R G S L R N L T S V V H N W T  
 N G K T L T L Q A S S S R Q S P V K S R H P H S M I P C  
 T E G R K L H P P N I A R A L P I K T F S G R Q T V E T T H C L Q S V

Dra I

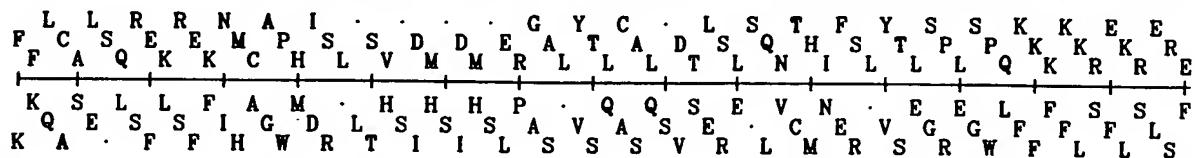
AAACTACCTACAGAGATTTAAAGCTCTAACGGTAAATATAAAATTTAACGGTATAATGTGTTAAACTACTGATTCTAAT 240  
 TTTGATGGATGTCTAAATTCTGAGATTCCATTATTTAAAAATTCAACATATTACACAATTGATGACTAAGATTA  
 Q T T Y R D L K L G K Y K I F K C I M C T T D S N  
 K L P L E I S S K V N I K F L S V C V K L L I L I  
 N Y L Q R F K A L R I N F V Y N V L N Y F  
 L S G V S I K F S P L Y I L I K L H I I H V V S E L  
 F R C L N L A R L Y I Y F K T Y L T N F Q N I N

TGTTTGTGTATTTAGATTCCAACCTATGGAACGTGATGAATGGGAGCAGTGGTGGAAATGCCCTTAATGAGGAAACCTGT 320  
 ACAAAACACATAAAATCTAACGGTTGGATACCTGACTACTAACCTCGTACCCACCTAACGGAAATTACTCCTTTGGACA  
 C V L C V I L D I S N L W N M G A V V E C L G K P V  
 L F V Y F R F Q P M E L M N G S S G G M A F P L M R K T C  
 Q K H I K S E L R H F Q H I P A C T T S H R H P F G T  
 N T Y K L N W G I S S I F F L L P P I G K I L S F F R Q N

FIG. 18A

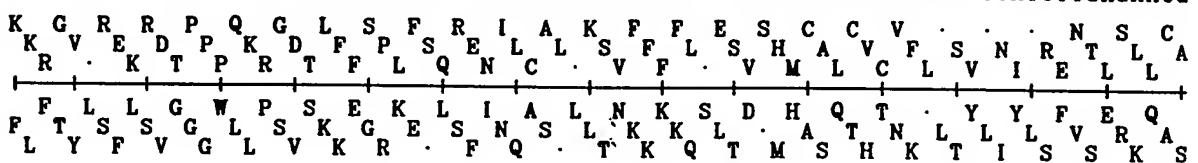
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TTTGCTCAGAAGAAATGCCATCTAGTGTATGAGGCTACTGCTGACTCTAACATTCTACTCCCTCCAAAAAGAAGAGA 400  
 AAACGAGTCTTCTTACGGTAGATCACTACTACTCCGATGACGACTGAGAGTTGTAAGATGAGGAGGTTTTCTCTCT

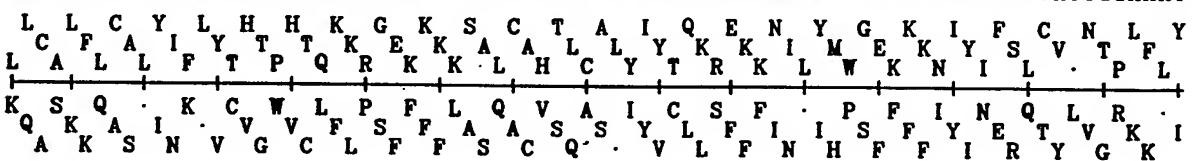


Sty I

AAGGTAGAAGACCCCAAGGACTTCTTCAGAATTGCTAAGTTTTGAGTCATGCTGTGTTAGTAATAGAACTCTTGC 480  
 TTCCATCTCTGGGGTTCCCTGAAAGGAAGTCTAACGATTCAAAACTCAGTACGACACAAATCATTATCTTGAGAACG

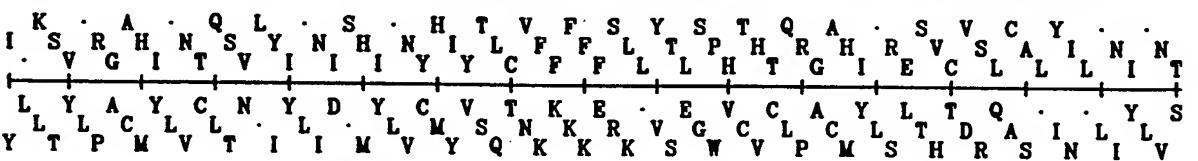


TTGCTTTGCTATTAACACCACAAAGAAAAAGCTGCACTGCTATAAGAAAATTATGAAAAAATATTCTGTAACCTTA 560  
 AACGAAACGATAAAATGTGGTCTTCTTCTGACGTGACGATATGTTCTTTAATACCTTTATAAGACATTGAAAT



Asel

TAAGTAGGCATAACAGTTATAATCATAACATACTGTTTTCTTACTCCACACAGGCATAAGAGTGTCTGCTATTAATAAC 640  
 ATTCCATCCGTATTGCAATATTAGTATTGTATGACAAAAAGAATGAGGTGTGTCCTATCTCACAGACGATAATTATTG



Rsa I

TATGCTAAAAATTGTGTACCTTAGCTTTAATTGTAAGGGGTTAATAAGGAATATTGATGTATAGTGCCTTGAC 720  
 ATACGAGTTTTAACACATGGAAATGAAAAATTAAACATTTCCCCAATTATTCTTATAAAACTACATATCACGGAACTG

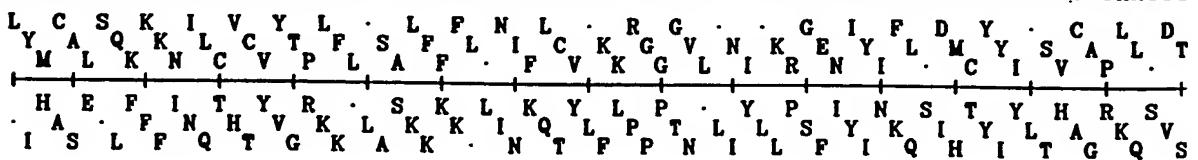


FIG. 18B

**BsaB I**  
**Dra I**  
TAGAGATCATAATCAGCCATACCAACATTGTAGAGGTTTACTTGCTTAAAAAACCTCCCACACCTCCCCCTGAACCTG  
ATCTCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTGGAGGGTGTGGAGGGGGACTGGAC 800

R S C G M C V S G V E P Q A P Q Q A E V C K A C I  
D L V E C V S V R V W K V P P R L P P Q Q A E V C K A C I  
I L W N V C Q L G C G K S P G S P A G R S M Q S M H  
L D Q P I H T L P T S L G W A G W C L A S T H A K H M  
S R T S H T D T L P T H F F D G P E G A P L L I C L M A D

**MfeI**  
**Hinc II**  
**Hpa I**

AAACATAAAATGAATGCAATTGTTGTTAACTTGTATTGCAAGCTTATAATGGTTACAAATAAGCAATAGCATCAC  
TTTGATTTACTTACGTTAACACAACAATTGAACAAATAACGTCGAATATTACCAATGTTATTCGTTATCGTAGTG 880

E N I K M Q L C L L T C L Q L I M V T N K A I A S  
K H K M N A I V V V N L F A A Y N G Y K S N S I T  
F M F H I C N N N V Q K N C S I I T V F L A I A D C  
F C Y F S H L Q Q S T L K N I A A L P L Y L L M V

**Xba I**

AAATTTCACAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGTCAAACCTCATCAATGTATCTTATCATGTCT  
TTTAAAGTGTATTTCGTAACACCAACAGGTTGAGTAGTTACATAGAATAGTACAGA 960

Q I S Q I K H F F H C I L V V V C P N S S M Y L T M S L  
K F H K S I F F T A F S L H S S C G L S K L I N V S Y H V  
N F T N K A F F S L H S S C G L S K L I N V S Y H V  
I E C I F C K K Q M R T T Q G F E D I Y R I M D H R  
L N L Y L M K K V A N . N H N T W V D L S M L T D T

**Sph I**  
**Nsi I**

AGATCTTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGGCTCCCCAGGCAGGAAGTATGCAAAGCATGCAT  
TCTAGAACACCTTACACACAGTCAATCCCACACCTTCAGGGTCCGAGGGTCCGTCTTCATACGTTACGTA 1040

R S C G M C V S G V E P Q A P Q Q A E V C K A C I  
D L V E C V S V R V W K V P P R L P P Q Q A E V C K A C I  
I L W N V C Q L G C G K S P G S P A G R S M Q S M H  
L D Q P I H T L P T S L G W A G W C L A S T H A K H M  
S R T S H T D T L P T H F F D G P E G A P L L I C L M A D

FIG. 18C

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Sph I  
Nsi I

CTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAAGTATGCAAAGCATGCATCTCAATTA 1120  
 GAGTTAACAGTCGTTGGTCCACACCTTCAGGGTCCGAGGGTCTGTCGTCTTCATACGTTCTGACGTAGAGTTAAT

Nco I  
Sty I

GTCAGCAACCATACTCCGCCCTAATCCGCCATCCGCCCTAATCCGCCAGTCCGCCATTCTCCGCCATG 1200  
 CAGTCGTTGGTATCAGGGCGGGATTGAGGCAGGGTAGGGCGGGATTGAGGCAGGGTAAGAGGCAGGGTAC

Bgl I  
Hae III Hae III Hae III

GCTGACTAATTTTTTTATTCAGAGGCCAGGCCCTCGGCCCTCTGAGCTATTCCAGAAAGTAGTGAGGAGGCTT 1280  
 CGACTGATTAAAAAAATAAATACGTCTCCGGCTCCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCCTCCGAAA

Hae III  
Stu I  
Avr II  
Sty I  
Ava I  
Xho I

TTTGGAGGCCTAGGCTTTGCAAAAGCTCCCTGAGACCTGGGTAATCATGGTATAGCTGTTCTGTGTAAATT 1360  
 AACCTCCGGATCCGAAACGTTTCGAGGGAGCTCGAACCCATTAGTACCAAGTATCGACAAAGGACACACTTAA

L E A F A K S S L E S L A S W S L F P V N  
 F W R P R L A K Q K A P S R A W R N H G H S C F L C E I  
 F G G L G F C K K L P R E L G V I M V I A V S C V K L  
 K S L A A K A F L E R S L K A Y D H D Y S N G T H F I Q  
 K P P R P K Q L F S G R S S P T I M T M A T E Q T F N

FIG. 18D

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BsrB I

~~GTTATCCGCTCACATTCCACACAACATACGAGCCGAAGCATAAAAGTGTAAAGCCTGGGTGCCTAATGAGTGAGCTAA~~ 1440  
~~CAATAGGCAGTGTAAAGGTGTTGATGCTCGGCCCTCGTATTTCACATTDGGACCCCACGGATTACTCACTCGATT~~  
~~C Y P L T I P H N I R A G S I K C K A W G A V S~~  
~~L S A H N S T Q H T S R K H K V S L G C L M S E L N~~  
~~T I G S V I G C L M R A P L M F H L A Q P A H T L~~  
~~N D A L E V C C V L R F C L T Y L R P H R I L S H A I V~~

Asel

Pvu II Asel Hae III

~~CTCACATTAATTGCGTTGCGCTCACTGCCGCTTCCAGTCGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA~~ 1520  
~~GAGTGTAATTAACGCAACGCGAGTGACGGCGAAAGGTCAGCCCTTGGACAGCACGGTCGACGTAATTACTTAGCCGGT~~  
~~L T L I A L R S L P A F Q S G N L S C Q L H I G Q~~  
~~T H I N C V A L T A R F P V G K P V V P A A C I L N E S A~~  
~~S V N I A N R E S G A K W D P F R D H W S C H I P W~~  
~~E C M L N R Q A S V A R K G T P F G T T G A A N I F R G~~

Sap I

~~ACCGCGGGGAGAGGCAGTTGCGTATTGGCGCTCTCCGCTCGCTCACTGACTCGCTGCCCTGGTCGTCGGC~~ 1600  
~~TGCGCGCCCTCTCCGCCAAACGATAACCCCGAGAAGGCGAAGGAGCGAGTGACTGAGGCCAGCGAGCCAGCAAGCCG~~  
~~R A G R G L R I G R S S A S L T D S L R S V V R~~  
~~T R G E R R F A V C V L G A L P L P R S L T R C A R S F G~~  
~~R A P L P P K R I P R E E A E E S V S E S R E T T R S~~  
~~V R P S L R N A Y Q A S K R K R A Q S A A S P R D N P A~~

BsrB I

~~TGCGGCAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAACATCAGGGATAACGAGGAAAGAACATG~~ 1680  
~~ACGCCGCTGCCATAGTCGAGTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCCTTCTGTAC~~  
~~L R R A V S A H S K A V I R L S T E S G D N A G K N M~~  
~~C G E R Y Q L T Q R R Y G Y P Q N Q G D I T Q E R E T H~~  
~~Q P R A T D A E F A T I R N D V S D P S L A P F F M~~  
~~A A L P I L E S L P P L V T I W L I L P Y R L F S C T~~

FIG. 18E

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### Hae III Hae III Hae III

1760  
TGAGC AAA AGGCCAGC AAA AGGCCAGGAACCGT AAAAAGGCCGTTGCTGGCGTTTCCATAGGCTCCGCCCTGA  
ACTCGTTTCCGGTCGTTCCGGTCCTGGCATTTCGGCGAACGACCGAAAAGGTATCGAGGCGGGGGACT

. A K G Q K R A P R N R K K A P A L L A F F H R L S R P P L D  
 V E S Q K K A P S K R P A K G Q E P . K G R V A G V F F S P I G L S A P P P P  
 H A C F P W C F A L F R L F A A N S Q A N K W L S R A G G R S V  
 S L C F A L L L G A F P W S G Y F P R T A Q P R T K G Y A E G A G G R Q

CCAGGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAACCCGACAGGACTATAAGATACCAGGGCTTCCCCCTG 1840  
GCTCGTAGTGT TTAGCTCGAGTTCTAGTCTCCACCGCTTGGGCTGTCTGATATTCTATGGTCCGAAAGGGGGAC

E S H H K N R R S V Q R W R N P T G L R D Y Q A F P P L  
 T R A S I T K I S D A Q V R G E T P R D Q R T I K D T R P R G V S P P L W  
 S C L F R R E L L H R F G V P S Y L V W A N G G R Q  
 R L M V F F I S A T D L P S A F G R S L V I F S V L P T K E G G R Q

GAAGCTCCCTCGCGCTCTCTGTTCCGACCTGCGGCTTACCGATAACCTGTCGCGCTTCTCCCTCGGGAAAGCGTG  
CTTCGAGGGAGCACCGCAGAGGACAAGGGTGGGACGGCGAATGGCTATGGACAGGGCGAAAGAGGGAAAGCCCTTCGAC 1920

GESPSLVRCPPLVPTLCPRLTGYLSPAPFLLSPRGEKARW  
 KALPPRCAALSLCSDPAAAYRIPVRLSPFGLKARW  
 LERTRERGTVRGSGVPSYRQDAKRGEGEPLATH  
 SFGGRASERQESGGAAARIRIGQTGRRKEREGLKPRFAARRH

## ApaL I

CGCCTTCTCAATGCTACGCTGAGGTATCTAGTCAGTCGGTGTAGTCGTCGCTCCAAGCTGGGCTGTGTGACGAACC  
CGCGAAAGAGTTACCGAGTGCACATCCATAGAGTCAGGCCACATCCAGCAAGGGAGGTTCCGACACACGTGCTTGG 2000

A L S Q C S R C R Y L S S V V V R S K L G C V H E P  
 R F L N A H A V G I S V R C R S F A P S W A V C T N  
 G A F S M L T L V S Q F G V G R S L Q A G L C A R T  
 A S E H E R Q L Y R L E T Y T T R E L S P Q T C S G G  
 R K R L A A T P I E T R H L D N A G L S Q P A T H V S F G G  
 A K E I S V S Y T D N P T P R E S W A P S H A R V

Nci I

CCCCGTTCA~~GGGG~~ACCGCTGCCCTATCCGTAAC~~T~~ATCGTCTGAGTCAACCCGTAAGACACGACTTATGCCAC 2080  
GGGGCAAGT~~GGGG~~CTGGCAGCGGAATAGGCCATTGATAGCAGAACTCAGGTGGGCCATTCTGTGCTGAATAGCGGTG

FIG. 18F

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Hae III

2160 TGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGGCGTGTACAGAGTTCTTGAAGTGGTGGCTAAC  
ACCGTCGGTACATTGCTTAATCGTCGGTCCATACATCCGCCACGATGTCTAAGAACCTCACCAACCGGATTG

TACGGCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTCGGAAAAAGAGTTGGTAGCTC  
ATGCCGATGTGATCTCTGTATTTAAACCATAGACGGAGACGACTCGGTCAATGGAAGCCTTTTCTCAACCATCGAG 2240

Y G Y T R R T V F G I C A L L K P V T F G K R V G S S  
 T A T L E G Q Y L V S A L C . S Q L P S E K E L V V A  
 R L H . K D S I W Y L R S A E A S Y L R K K S W . L  
 P V L L V T N P I Q A R S F G T V K P F L T P L E  
 V A V S S P C T Y K T D A S Q F L W N G E S F S N T A R  
 R S C . F S L I Q Y R R E A S A L . R R F F L Q Y S

TTGATCCGGAAACAAACCCGGCTGGTAGCGGTGGTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGAT 2320  
AACTAGGGCGTTGTTGGTGGCACCATGCCACCAAAAAACAAACGTTCTGTCGTCTAATGCGCGTCTTTTCTA

· S G K Q T T A G S G G F F V C K Q Q I T R R K K G  
L D P A N K P L V A V V F F L F C L Q A S R L Y R A E K K K K R D  
L I R Q T N H R W R W F F C L Q A A D Y A Q K K K R I  
|  
Q D P L C V V A P L P P K K T Q L C C I V R L F F P D  
S G A F L G G S T A T T K K T N A L L N R A C S F F P D  
K I R C V F W R Q Y R H N K Q K C A A S A C F F P L I

## BspH I

CTCAAGAAGATCCTTGATCTTCTACGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTGGTCATG 2400  
GAGTTCTCTAGGAAACTAGAAAAAGATGCCAGACTGCGAGTCACCTGCTTTGAGTGCATTCCCTAAACCAAGTAC

S Q E D P L I F S T G S D A Q W N E N S R G I L V M  
 L K K I L S F L R G L T L S G T K T H V K G F W S H  
 S R R S F D L F Y G V R S V E R K L T L R D F G H  
 S S G K I K E V P D S A H F S F E R P I K T M  
 R L F I R Q K R R P R V S L P V F V T L P N Q D H S  
 E L L D K S R K P T Q R E T S R F S V N L S K P

Dra I

Dra I

AGATTATCAAAAGGATCTCACCTAGATCTTTAAATTAAAAATGAAGTTAAATCAATCTAAAGTATATATGAGTA 2480  
TCTAATAGTTTCTAGAAGTGGATCTAGGAAAAATTAACTTACTCTAAAAATTAGTTAGATTCTATATACTCAT

R L S K R I F T I L L N K S F K S I S I Y E  
 D Y Q K G S P R S F I K N E V L N Q S K V Y M S  
 E I I K K D L H L D P F K L K M K F I N L K Y I V  
 L N D F L I K V I R K F F H L K L D I L I Y S Y  
 S I I L F S R R S G K L I N F I S T K F I D L T Y I H T

FIG. 18G

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AACTTGGTCTGACAGTTACCAATGCTTAATCACTGAGGCACCTATCTCAGCGATCTGTCTATTCGTTATCCATAGTTG  
 TTGAACCAGACTGTCATGGTTACGAATTAGTCACTCCTGGATAGAGTCGCTAGACAGATAAAAGCAACTAGGTATCAAC 2560

T W S D S Y Q C L I S E A P I S A I C L F R S S I V  
 K L G L T V T P N A S V R H L S Q R S V Y F V H P L  
 N L V Q L P M L N Q G T Y L S D L S I S F I H S C  
 V Q D S L W H K I L S A G I E A I Q R N R E D M T A  
 S P R V T V L A D T L C R D R D T K T E N M W L Q  
 F K T Q C N G I S L H P V R L S R D I E N M W L Q

Hae III

CCTGACTCCCCGTCTGCTAGATAACTACGATAACGGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATAACCGCAGAC 2640  
 GGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCGAATGGTAGACCGGGGTACCGACGTTACTATGGCGCTCTG

A D L P V V I T T I R E G L P S G P S A A M I P R D  
 P D S P S C R I T R Y G R A L Y H L A P V A L Q M Y R E T  
 L T P R R V D N Y D T G G L T I W P Q C C N D T A R  
 Q S E G T T Y I V V I R S P K G D P G L A A I I G R S  
 G S E G D H L Y S R Y P L A W R A G T S C H Y R S V  
 R V G R R T S L S V P P S V M Q G W H Q L S V A L G

Bgl I

Hae III

Ava II

CCACGGCTCACCGGCTCCAGATTATCAGCAATAAACAGCCAGCCAGGGAGGGAGAAGTGGCTCTGCAACTT 2720  
 GGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTGGTCGGCTCCGGCTCGCTTACCAAGGACGTTGAA

P R S P A P D L S A I N Q P A G R A E R R S G P A T L  
 H A H R L Q I Y Q Q T S Q P E G P S A E V V L Q N L  
 P T L T G S R F I S N K P A S R K G R A Q K W S C N F  
 G R E G A G S K D A I F W G A P L A S R L L P G A V K  
 W A R S W I C Y V L W G S P G L A S T T R C S T R C S K  
 V S V P E L N I L L G A L R F P R A C F H D Q L K

Asel

Nci I

Fsp I

ATCCGCCTCCATCCAGTCTATTAAATTGTCGGGGAAAGCTAGAGTAAGTAGTTGCCAGTTAATAGTTGGCAACGTTG 2800  
 TAGGCGGAGGTAGGTCAAGATAATTAACAACGGCCCTTCGATCTCATTCAAGCGGTCAATTATCAAACGGTGTGCAAC

S A P S I Q S I N C C R E A R V S S P V N I S L R N V  
 Y P P P S S L I V A G K L E V V V R Q L I V C A T L  
 I R L H P V Y L L P G S S K F A S F A Q R C  
 D A E M W D I L Q Q R S A L T L L E G T L L K R L T T  
 G G G D L R N I T A P F S S Y T T R W N I T Q A V N  
 I R R W G T N N G P L L L Y N A L Y N A C R Q

TTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTGGTATGGCTTCAATTAGCTCCGGTCCAAACGATCAAGG 2880  
 AACGGTAACGATGTCCGTAGCACACAGTCGCGAGCAGCAACCATACCGAAGTAAGTCGAGGCCAACGGTTGCTAGTTCC

V A I A T G I V V S R S S F G M A S F S S G S Q R S R  
 L P L L Q A S W C H A R R L V W L H S A P V P N D Q R  
 C H C Y R H R G V T L V V W Y G F I Q L R F P T I K  
 N A M A V P M T D R E D N P I A E N L E P E W R D L  
 Q W Q S C A D H H T A R R K T H S E A G T E W R D L  
 L C R P T V S T T Q Y P K M S R N G V I L A

FIG. 18H

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<p>CGAGTTACATGATCCCCCATGTTGTCAAAAAAGCGGTTAGCTCCTCGTCCCTCGATCGTTGTCAAGAAGTAAGTTGGC          GCTCAATGTAAGGGGGTACAACACGTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCG</p> <p>R V T D S P M C L C K K A V S S F G P P I V V R S K L A          E L H D P P C V A K K R L A P S V L R S D S L R C Q K V S W          A S Y M I P H V V Q K S G L L R S S D R C Q K V S W          R T V H D G M N H L F A T L E K P G G I T T L L L N A          S N C S G G H Q A F F R N A G E T R R D N D S T L Q G          L M I G W T T C F L P S R R D E S R Q F Y T P</p> <p>CGCAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTATGCCATCCGTAAGATGCTTTCTGTGA          GCGTCACAATAGTGAATACCAATACCGTCGTACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACT</p> <p>P A V L S L M V M A A L H N S L T V M P S V R C F S V          Q C Y H S W L W Q H C I I L L S C H P D A F L          R S V I T H G Y G S T A F S Y C H A I R K M L F C D          A T N D S M T I A A S C L E R V T M G D T L H K E T V          C H T I V E H N H C A S Q M I R K S D H W G Y S A K R H S          R L T P P L V A Y N E Q A M R L I S K Q S</p>	<p>Ava II      Pvu I      Hae III</p>
<p>Rsa I          Sca I</p> <p>CTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGGCGACCGAGTTGCTTTGCCCGCGTCAACACGGGAT          GACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTAACGAGAACGGGCCGAGTTGTGCCCTA</p> <p>T G E Y S T K S F E C M R R P S C P A S T R D          L V S T Q P S H S E N S V C G D R V A L L A R Q H G I          W V L N Q V I L R I V Y A A T E L L L A P G V N T G          P S Y E V L D N Q S Y H I R R G L Q E Q G A D V R S          S T L V G L D N E S Y F L T H P S R T A R A R P T L V P I Y          Q H T S L W T M R L I T Y A A V S N S K G P T L V P I Y</p>	<p>Nci I      Hinc II</p>
<p>Dra I          Xmn I</p> <p>AATACCGGCCACATAGCAGAACTTAAAAGTGTATCATATTGGAAACGTTCTCGGGCGAAACTCTCAAGGATCTT          TTATGGCGCGGTGTATCGTCTTGAAATTTACCGAGTAGTAACCTTTGCAAGAACCCCCGTTTGAGAGTTCCCTAGAA</p> <p>N T A P H I S R T L K V L I I G K R S S G R K L S R I L          I P R H I A E L K K C S H S L E N V L R G R K L S Q G I L          Y R A T Q N F K S A H H W K T F F G A K T L K D L          L V A G C L L V K F T S M M P F R E E P R F S E L P I K          I Y G R W M A S S K F H E D N S F T R P A S F V E L P D R</p>	<p>3200</p>

FIG. 18I

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Apal I

ACCGCTGTTGAGATCCAGTCGATGTAACCCACTCGTCACCCAACTGATCTTCAGCATCTTTACTTCAACCAGCGTTT 3280  
 TGGCGACAACCTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAAGTCGTAGAAAATGAAAGTGGTCGCAAA

P L L R S S M P T R A P N S S A S F T T S V  
 Y R C D P V R C N P L V H P T D L Q H L L S P A F  
 T A V E I Q F D V T H S C T Q L I F S I F Y F H Q R F  
 G S N L D L E I Y G V R A G L Q D E A D K V K V L T E  
 Y R Q Q S I G T R H L G S T C G V S R E A D K V K V L T E  
 V A T S I W N S T V W E H V W S I K L M K . K . W R K

CTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTC 3360  
 GACCCACTCGTTTTGTCCTCGTTTACGGCGTTTTCCCTTATTCCCGCTGTGCCCTTACAACTTATGAGTATGAG

S G A K T G R Q N A A K K G I R A T R K C I L I L  
 L G E Q K Q E G K M P Q K R G E N G R H G K C I L I L  
 W V S K N R K A K C R K K G N K G D T E M L N T H T  
 P H A F V P L C F A A F F P I L A V R F H Q I S M S  
 R P S C F C S P L I G C F L P S Y P R C P F H Q I S M S  
 Q T L L F L F A F H R L F P F L P S V S I N F V Y E V R

Hinc II Spe I Asel

TTCCTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCATGCGCGTTGACATTGATTATTGACTAGTTATTAA 3440  
 AAGGAAAAAGTTATAATAACTTCGTAATAGTCCCATAACAGACTACGGCGACTGTAACTAATAACTGATCAATAATT

F L F Q Y Y S I Y Q G Y C L M R V D I D Y D L V I N  
 S F F N Y I L I E A I Y Q G Y C L M R V D I D Y D L V I N  
 L P F S I L L K H L S G L Y S H A R . H . L L T S Y .  
 K R K Y Q L M P Q R M R T S M S Q S T I L  
 E K K L I I S A N I L P T I T E H A N V N I S N N I

Hae III Bgl I

TAGTAATCAATTACGGGTCAATTAGTTCATAGCCCATAATGGAGTTCCCGCTTACATAACTTACGGTAAATGGCCCGCC 3520  
 ATCATTAGTTAATGCCCGACTAATCAAGTATCGGTATATACCTCAAGGCGCAATGTATTGAATGCCATTACGGCGG

S N Q L R G H F I A H I W S S A L H N L R M A R  
 I V I N Y G V I S H P I Y G V S P R Y I T L Y G K W P A P  
 I S I T G S I L V H S P Y M E F R V T L T V N G P P A P  
 L L I N R P N M A W I H L E A N C L K R Y I A R R  
 Y Y D I V P D N T E Y G M Y P T G R M V P L H G G A G

FIG. 18J

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Aat II

TGGCTGACCGCCCAACGACCCCCCCCCATTGACGTCAATAATGACGTATGTTCCATAGTAACGCCAATACGGACTTCC  
 ACCGACTGGCGGGTTGCTGGGGCGGGTAAGTGCAGTTATTACTGCATACAAGGGTATCATTGCGTTATCCCTGAAAGG 3600  
 W A D R P T T P A H R Q R M F P R Q G L S  
 W L T A Q R P P P P I D V N N D V C S H S N A N R D F P  
 G P P N D P P R P L T S I M T Y V P I V T P I G T F  
 Q A S R G V V G A W Q R I N G Y Y R W Y P S E  
 P S V A W R G G M S T L L S T H E W L L A L I L S V K G  
 P Q G G L S G R G N V D I I V Y T G M T V G I P V K W

Aat II

Bgl I

Rsa I

Nde I

Rsa I

ATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCACTTGGCACTACATCAAGTGTATCATATGCCAAGTACGGCC  
 TAAGTGCAGTTACCCACCTGATAAAATGCCATTGACGGGTACCGTCACTGAGTTACATAGTATACGGTTCATGCGGG 3680  
 I D T V N G W T I Y G K L P T W Q Y I K C I C Q V R P  
 H L T S M G G L F T V N C P L G S T S S V Y A K Y A P  
 H R Q W V D Y L R T A H L A V H Q V Y H M P S T P  
 M S T L P H V I P L S G V Q C Y M L H I M H W T R G  
 N V D I P P S N V T F Q G S P L V D L T Y D Y A L Y A G  
 Q R H T S K R Y V A W K A T C T Y I G L V G

Hae III

Aat II

Bgl I

Rsa I

CCTATTGACGTCAATGACGGTAAATGGCCCGCTGGATTATGCCAGTACATGACCTTATGGGACTTTCTACTTGGCA  
 GGATAACTGCAGTTACTGCCATTACGGGGGGACCGTAATACGGGTACGTACTGGAATACCCCTGAAAGGATGACCGT 3760  
 P L L T S M T V N G P P G I M P S T P Y G T F L L G  
 P I D V N D G K W P A R L A L C P V H D L M G L F S Y L A Q  
 R N V D I V T F P G G P M I G L V H G P V K R S P A L  
 G I S T L S P L H G A Q C A W Y M V K H S K G V Q A C

BsaA I

Nco I

Rsa I SnaB I

Sty I

Rsa I

GTACATCTACGTATTAGTCATCGCTATTACCATGGTATGCCGTTTGGCAGTACATCAATGGCGTGGATAGCGGTTG  
 CATGTAGATGCATAATCACTAGCGATAATGGTACCACTACGCCAAACCGTCATGTAGTTACCCGCACCTATGCCAAAC 3840  
 S T S T Y S S L L P W C G F G S T S M G V D S G L  
 V H L R I S H R Y H G D A V F L A V H Q W A W D I A V  
 Y I Y V L V I A I T M V M R F W Q Y I N G R G R F  
 T V D V Y D D S N G H H P K P L V D I P T S L P K  
 T C R R I L D D S N G H H P K P L V D I P T S L P K  
 T M T N T M A I V M T I R N Q C Y M L P R P Y R N S

FIG. 18K

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Aat II

ACTCACGGGGATTCAGTCTCCACCCATTGACGTCAATGGGAGTTGTTGGCACCAAAATCAACGGGACTTCCA  
 TGAGTCCCCCTAAAGGTTAGAGCTGGGTAAGTGCAGTTACCCCTAAACAAACCGTGGTTAGTTGCCCTGAAAGGT 3920  
 T H G D I F Q V S P T P L T S M G V C F G A T P K I N G T F Q  
 D L T G I S K S P H P I D V N G S L F W H Q N Q R D L F S P  
 V P S K W T E V G N V D I P T Q K P V L I L P V K W  
 S V P I E L D G G W Q R H S N T K A G F D V P S K E L  
 E R P N G L R W G M S T L P L K N Q C W F R S K G

Rsa I

Sac I

AAATGTCGTAACAACCTCCGCCCATGACGCAAATGGCGGTAGGGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCT 4000  
 TTTACAGCATTGTTAGGGGGGTAAGTGCCTTACCCGCCATCCGCACATGCCACCCCTCCAGATATATTCTCGAGA  
 N V V T P P H R K W A V G V Y G G R S I A E L  
 K M S . Q L R P I D A N G R A C V T V G E G L Y K Q S S  
 K C R N N S A P L T Q M G G R R V R W E V Y I S R A L  
 F I D T V V G G W Q R L H A T P T Y P P L D I Y A S S E  
 F H R L L E A G N V C I P P L R T R H S T I L C L A R

Age I

CTGGCTAACTAGAGAACCCACTGCTTAACCTGGCTTATCGAAATTAAACGACTCACTATAGGGAGACCC  
 GACGGATTGATCTTGGGTGACGAATTGACCAATAGCTTAAATTATGCTGAGTGATATCCCTCTGGG 4069  
 S G L E N P L L N W L I E I N T T H Y R E T  
 W L T R E P T A L H C L T G L S K L I R L T I G R E T  
 P A S S F G S S L Q S I S I L V V . L S V W  
 R Q S V L S G V A S A R F N I R S V I P L S G G

FIG. 18L